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# FIGURE 1

1	AGCTCCAGCCTAGGCGTTCTACCTGGAAGAATGCAGGGGCCAGTACCTAGGACTGAGGA	60
61	AGATGGCTGACATCCAGAACATTTTCGTGGACAGCCAGGAGCGTAGGGCTGTGGCAG	120
121	TGCCCTGTGATCTTTGCCCTCATCTTCTGTGGCATGTTGGCAATGGGCTGGTGTGG	180
181	CTGTGCTACTGCAGCCTGGCCCAAGTGCCCTGGCAGGAGCCAAAGCAGTACCACAGATCTCT	240
241	TCATCCTCAACTTGGCCGTGGCCGACCTTTTGTTCATCTGTGCTGCGTGCCCTTCCAGG	300
301	CAGCCATCTACACACTGGATGCCCTGGCTCTTTGGGCTTTCGTGTGCAAGACGGTACATC	360
361	TGCTCATCTACCTACCATGTATGCCAGCAGCTTCACTGCGGCGCTTCTCCCTGGACA	420
421	GGTACCTGGCTGTGGGCACCCACTGCGCTCCAGAGCCCTGCGCACCCCGCAACGCGC	480
481	GCGCCGCGGTGGGCTCGTGTGGCTGTGGCGCTCTTTCCTCCGCGCTTACCTAAGCT	540
541	ATTACGGCACGGTGGCTACGGCGCGCTCGAGCTCTGCGTGCCCGCTTGGAGGACGCGC	600
601	GGCGGCGCGCTGGACGTGGCCACCTTCGCCGCGGCTACCTGCTGCCGCTGGCGCTGG	660
661	TGAGCCTGGCCTACGGACGACGCTATGTTTCTATGGGCCCGCGTGCGTCCCGCGGCG	720
721	CGCGGCGCAGCAGAGCGCGCAGACGGCGACCGCGCGGCGGACGCGCCATGCTGGCAG	780
781	TGGCCGCGCTCTACGCGCTTTGCTGGGCGCCGACACCGCGCTCATCTCTGCTTCTGGT	840
841	ACGGCCGCTTCGCCCTTCAGCCCGGCCACCTACGCTGTGCGCTGGCTCGCACTGCCCTCG	900
901	CCTACGCCCAACTCCTGCCCTTAACCGCTCGTCTACTCGCTCGCTCGCGCCACTTCCGCG	960
961	CGCGCTTCCGCGCGCTGTGGCCCTGCGGCGCTCGCGCCACCGCCACACCGCGCTC	1020
1021	ATCGAGCCCTCCGTCGTGTCCAGCCGCGCTTTCGGGCCCGCGGTTATCCCGCGGACG	1080
1081	CCAGGCCCTCGTGTGGAGTATGGAGCCAGAGGGGATGCTCTGCGTGGTGGAGAGA	1140
1141	CTAGACTAACCTGTCCCCCAGGGACCTCAATAAACCCTGCCCGCTTGGACTCTGACGTC	1200
1201	TGTCAGAAATGCCACCAAGGAACATCTAGGGAACGGCAGTCTCGCCAGGCTCCACCAAAA	1260
1261	GCAGAAGCAAAGTTGCAGGG	1280

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20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 370

V A F A L R R Y R V A V Y A A H A T  
A L L Q H D A S A V G A W L R A D E  
V V D F V L N L D A A L F C F R G G  
A L T P T S R Y E V P M C H H H P G  
G G T V K V P P W P G A L S R H Y G  
V N S C C A T A A L V R I A S H G R  
S G S C V A R S P L A G L L A R A L  
G V P L F L L F V Y A A A R L H P A  
P M E I A T A L C G W R H C S R G D  
S G Q F G F R A L A L G H A Y R S G  
D L W C F S S A E A F T P Y V R S R Q  
L L A L L S R L L F C A G T L G A P P  
S F S D W A L L A T L R W A P C P E G  
I I P A A Y P W G A T R C P N P Q M R  
N L G V D M H V Y V R R L S L W V S P  
Q A P A L T R L R D G A A F C L R W S  
I F Q L T L V G V L Y E Y A S R R G L  
D I L N Y Y A V T A A A L F N R L R T  
A V L L I I L A G R L A A R A F A P L  
M P V I A L Y A Y R S A A G Y R R R R

1 21 41 61 81 101 121 141 161 181 201 221 241 261 281 301 312 341 361

FIGURE 2

202F40" CHE900T

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# FIGURE 3

1	CACTCAGCGATGAC	60
61	AGAACACCTGGCCAGAC	120
121	GGGGGCTCTTGCCCTGAGGAT	180
181	GCTGATGCCCAGAACAT	240
241	GTGGTCTTTGCCCCAAT	300
301	CTCCTGCAGCCTGGCCGAGT	360
361	CTCAACCTGGCGGTGGCTGAC	420
421	ATCTACACGCTGGATGCCCTGG	480
481	ATCTACCTCACCATGTACGCCAG	540
541	CTGGCCGTGGGCAACCGCTGCG	600
601	GCAGTGGGCCTGGTGGCTGG	660
661	GGACCCGTGCGCTACGGCGCTG	720
721	CGCGCCCTGGACGTGGCCACCT	780
781	CTGGCCCTACGGCGCACGCTGCG	840
841	GCGGCCGAGGCGCGGAGGCGG	900
901	GCGCTCTACGCGCTCTGCTGGG	960
961	CGCTTCGCCCTTCAGCCCGGCA	1020
021	GCCAACTCCTGCCCTCAACCCG	1080
081	TTCCGCCCGCTGTGGCCGTGCG	1140
141	CGCGTCCGCCCGCGTCTCGGG	1200
201	AGGCTGCTGGCTGTGGCGGCC	1260
261	GAGGCTGCCCGAGGACCGGAAT	1320
321	TCACTCCCGTTCTCCGAAGCGG	1380
381	TCCTCTAGGGGCGTTGAGTGG	1417

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FIGURE 4

1	H	S	A	M	T	L	A	Q	L	V	L	A	L	V	P	L	L	S	G	S	P	R	P	S	R	S	F	T	Q	20
21	R	T	P	G	Q	R	I	I	G	P	L	L	L	G	V	C	L	L	A	E	G	G	P	C	V	N	E	T	R	40
41	G	D	S	A	L	A	I	I	N	A	L	L	L	F	A	G	L	L	A	L	L	L	L	L	L	L	L	L	L	60
61	A	V	F	Q	P	A	A	S	D	W	A	L	L	F	A	G	L	L	A	L	L	L	L	L	L	L	L	L	L	80
81	V	L	N	Y	L	T	L	Y	Y	A	V	T	A	A	A	L	F	N	R	V	L	A	R	E	R	R	R	R	R	100
101	L	L	I	I	L	A	G	R	L	G	V	L	Y	E	A	Y	A	S	R	R	L	A	R	E	R	R	R	R	R	120
121	L	I	I	L	A	G	R	L	G	V	L	Y	E	A	Y	A	S	R	R	L	A	R	E	R	R	R	R	R	R	140
141	I	I	L	A	G	R	L	G	V	L	Y	E	A	Y	A	S	R	R	L	A	R	E	R	R	R	R	R	R	R	160
161	I	I	L	A	G	R	L	G	V	L	Y	E	A	Y	A	S	R	R	L	A	R	E	R	R	R	R	R	R	R	180
181	L	A	V	T	A	A	A	L	F	N	R	V	L	A	R	E	R	R	L	A	R	E	R	R	R	R	R	R	R	200
201	A	G	R	L	G	V	L	Y	E	A	Y	A	S	R	R	L	A	R	E	R	R	L	A	R	E	R	R	R	R	220
221	G	R	L	G	V	L	Y	E	A	Y	A	S	R	R	L	A	R	E	R	R	L	A	R	E	R	R	R	R	R	240
241	R	L	A	A	L	F	N	R	V	L	A	R	E	R	R	L	A	R	E	R	R	L	A	R	E	R	R	R	R	260
261	L	A	A	L	F	N	R	V	L	A	R	E	R	R	L	A	R	E	R	R	L	A	R	E	R	R	R	R	R	280
281	A	A	L	F	N	R	V	L	A	R	E	R	R	L	A	R	E	R	R	L	A	R	E	R	R	R	R	R	R	300
301	A	A	L	F	N	R	V	L	A	R	E	R	R	L	A	R	E	R	R	L	A	R	E	R	R	R	R	R	R	320
321	A	A	L	F	N	R	V	L	A	R	E	R	R	L	A	R	E	R	R	L	A	R	E	R	R	R	R	R	R	340
341	A	A	L	F	N	R	V	L	A	R	E	R	R	L	A	R	E	R	R	L	A	R	E	R	R	R	R	R	R	360
361	A	A	L	F	N	R	V	L	A	R	E	R	R	L	A	R	E	R	R	L	A	R	E	R	R	R	R	R	R	380
381	A	A	L	F	N	R	V	L	A	R	E	R	R	L	A	R	E	R	R	L	A	R	E	R	R	R	R	R	R	400
401	A	A	L	F	N	R	V	L	A	R	E	R	R	L	A	R	E	R	R	L	A	R	E	R	R	R	R	R	R	420
421	A	A	L	F	N	R	V	L	A	R	E	R	R	L	A	R	E	R	R	L	A	R	E	R	R	R	R	R	R	440

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# FIGURE 5A

hGALR3	. . . . .	M A D A Q N I S L D S P G . . . . .	13
rGALR3	. . . . .	M A D I Q N I S L D S P G . . . . .	13
rGALR1	M E L A P V N L S E G N G S D P E P P A E P R P L		25
hGALR3	. . . . .	S V G A V A V P V V F A L I F L L G T V G N	35
rGALR3	. . . . .	S V G A V A V P V I F A L I F L L G M V G N	35
rGALR1	F G I G V E N F I T L V V F G L I F A M G V L G N		50
hGALR3	G L V L A V L L Q P G P S A W Q E P G S T T D L F		60
rGALR3	G L V L A V L L Q P G P S A W Q E P S S T T D L F		60
rGALR1	S L V I T V L A R S K P G . . . K P R S T T N L F		72
hGALR3	I L N L A V A D L C F I L C C V P F Q A T I Y T L		85
rGALR3	I L N L A V A D L C F I L C C V P F Q A A I Y T L		85
rGALR1	I L N L S I A D L A Y L L F C I P F Q A T V Y A L		97



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FIGURE 5C

hGALR3	A	L	D	V	A	T	F	A	A	G	Y	L	L	P	V	A	V	V	S	L	A	Y	G	R	T	207	
rGALR3	A	L	D	V	A	T	F	A	A	G	Y	L	L	P	V	A	V	V	S	L	A	Y	G	R	T	207	
rGALR1	A	Y	V	V	C	T	F	V	F	G	Y	L	L	P	L	L	I	C	F	C	Y	A	K	V	221		
V																											
hGALR3	L	R	F	L	W	A	A	V	G	P	A	G	A	A	A	E	A	R	R	R	A	T	G	R	232		
rGALR3	L	C	F	L	W	A	A	V	G	P	A	G	A	A	A	E	A	R	R	R	A	T	G	R	232		
rGALR1	L	N	H	L	H	K	K	L	K	N	M	S	K	K	S	E	A	S	K	.	.	.	.	K	242		
VI																											
hGALR3	A	G	R	A	M	L	A	V	A	A	L	Y	A	L	C	W	G	P	H	H	A	L	I	L	C	257	
rGALR3	A	G	R	A	M	L	A	V	A	A	L	Y	A	L	C	W	G	P	H	H	A	L	I	L	C	257	
rGALR1	T	A	Q	T	V	L	V	V	V	V	V	F	G	I	S	W	L	P	H	H	V	I	H	L	W	267	
VII																											
hGALR3	F	W	Y	G	R	F	A	F	S	P	A	T	Y	A	C	R	L	A	S	H	C	L	A	Y	A	282	
rGALR3	F	W	Y	G	R	F	A	F	S	P	A	T	Y	A	C	R	L	A	S	H	C	L	A	Y	A	282	
rGALR1	A	E	F	G	A	F	P	L	T	P	A	S	F	F	F	R	I	T	A	H	C	L	A	Y	S	292	

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# FIGURE 5D

hGALR3	N	S	C	L	N	P	L	V	Y	A	L	A	S	R	H	F	R	A	R	F	R	R	L	W	P	307
rGALR3	N	S	C	L	N	P	L	V	Y	S	L	A	S	R	H	F	R	A	R	F	R	R	L	W	P	307
rGALR1	N	S	S	V	N	P	I	I	Y	A	F	L	S	E	N	F	R	K	A	Y	K	Q	V	F	K	317
hGALR3	C	G	R	R	R	.	.	.	R	H	R	A	R	R	A	L	R	R	V	R	P	A	S	S	G	329
rGALR3	C	G	R	R	R	H	R	H	H	R	A	H	R	A	L	R	R	V	Q	P	A	S	S	G	332	
rGALR1	C	R	V	C	N	E	S	P	H	G	D	A	K	E	K	N	R	I	D	T	P	P	S	T	N	342
hGALR3	P	P	G	C	P	G	D	A	R	P	S	G	R	L	L	A	G	G	Q	G	P	E	P	R	354	
rGALR3	P	A	G	Y	P	G	D	A	R	P	R	G	W	S	M	.	.	.	.	.	.	E	P	R	350	
rGALR1	C	T	H	V	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	346	
hGALR3	E	G	P	V	H	G	G	E	.	.	.	.	.	.	A	A	R	G	P	E	.	.	.	368		
rGALR3	G	D	A	L	R	G	G	E	T	R	L	T	L	S	P	R	G	P	Q	.	.	.	.	370		



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FIGURE 6A

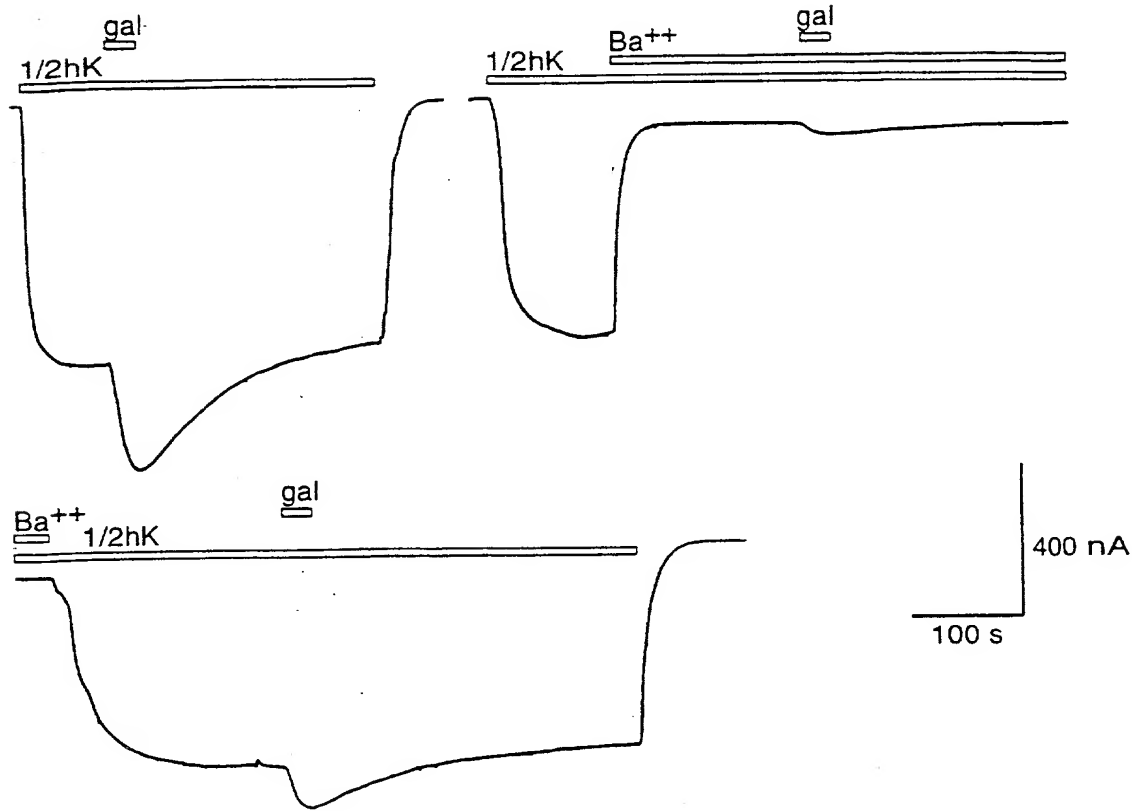
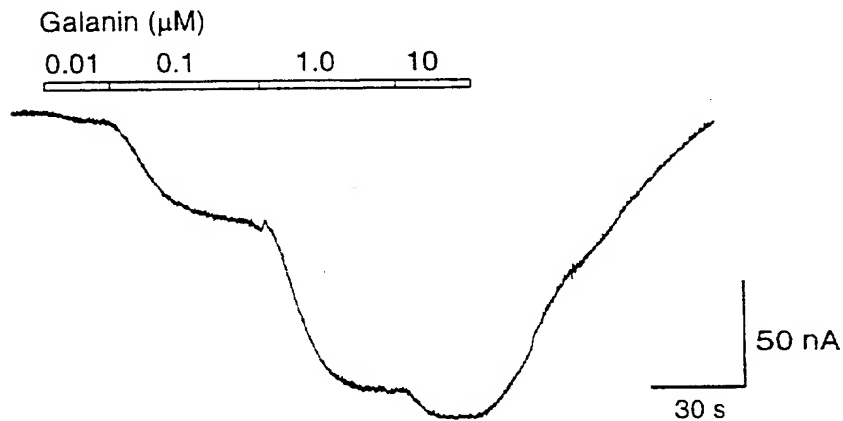


FIGURE 6B



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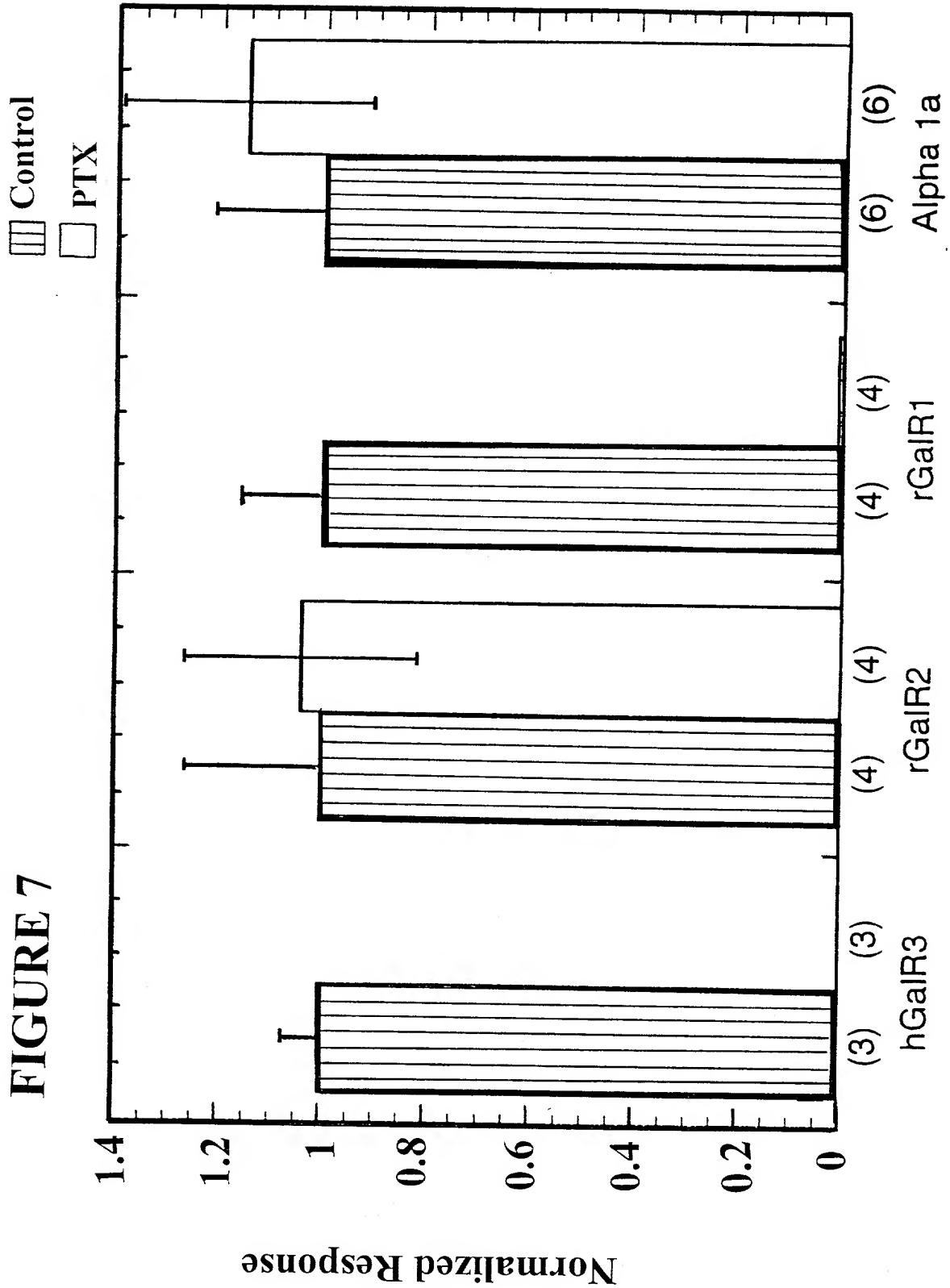


FIGURE 8A

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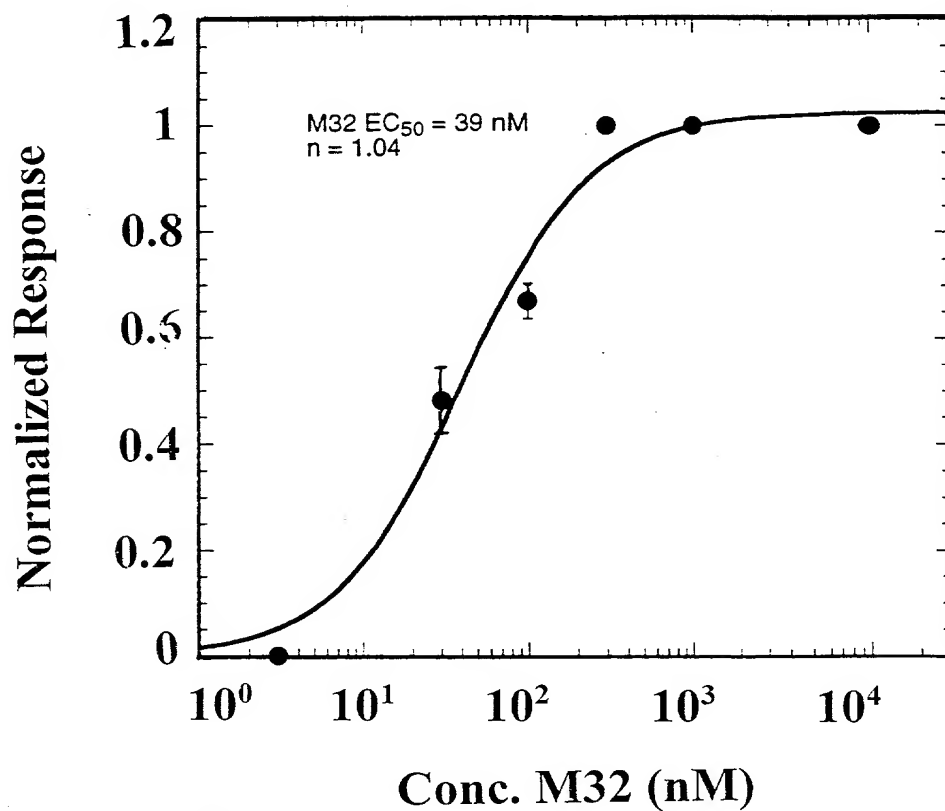
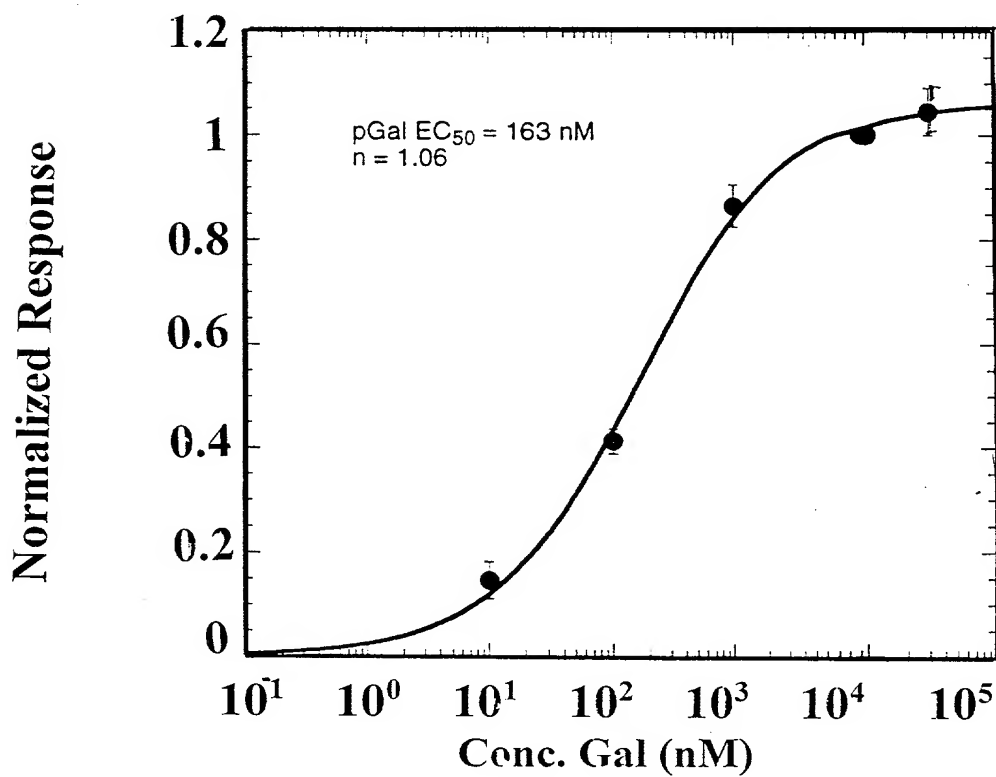
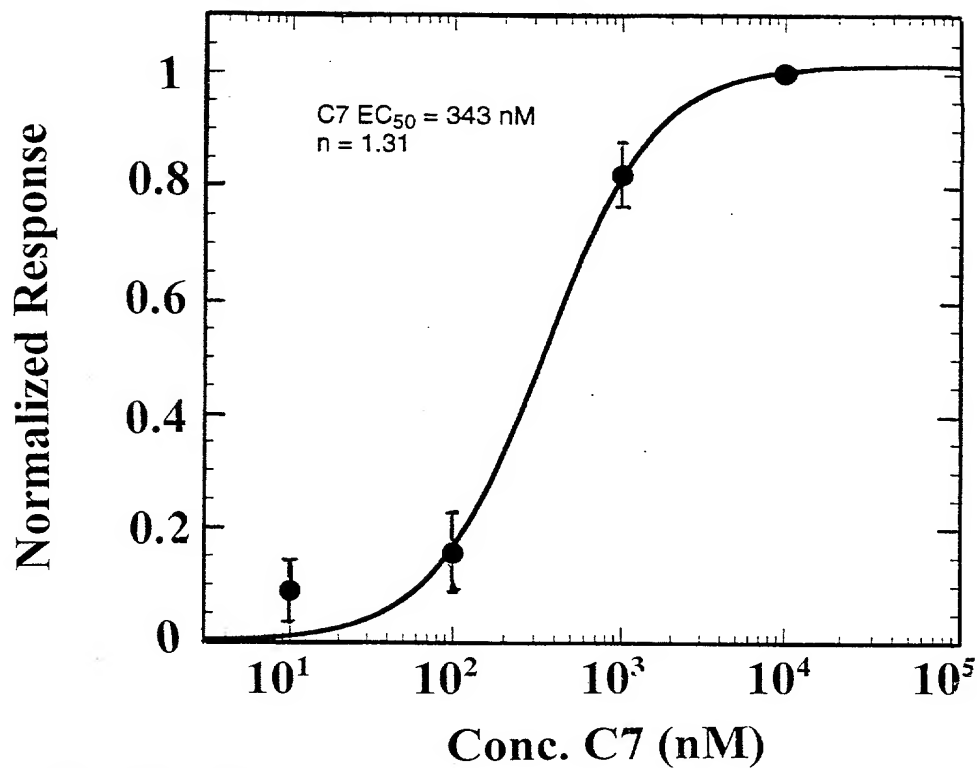


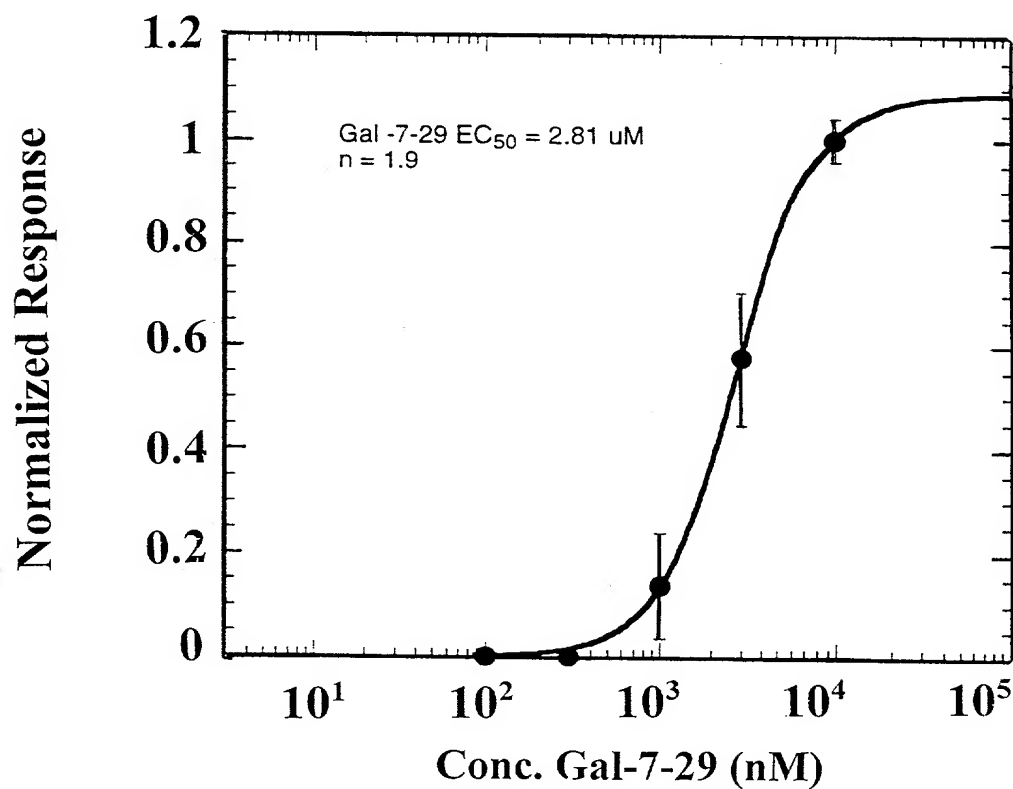
FIGURE 8B



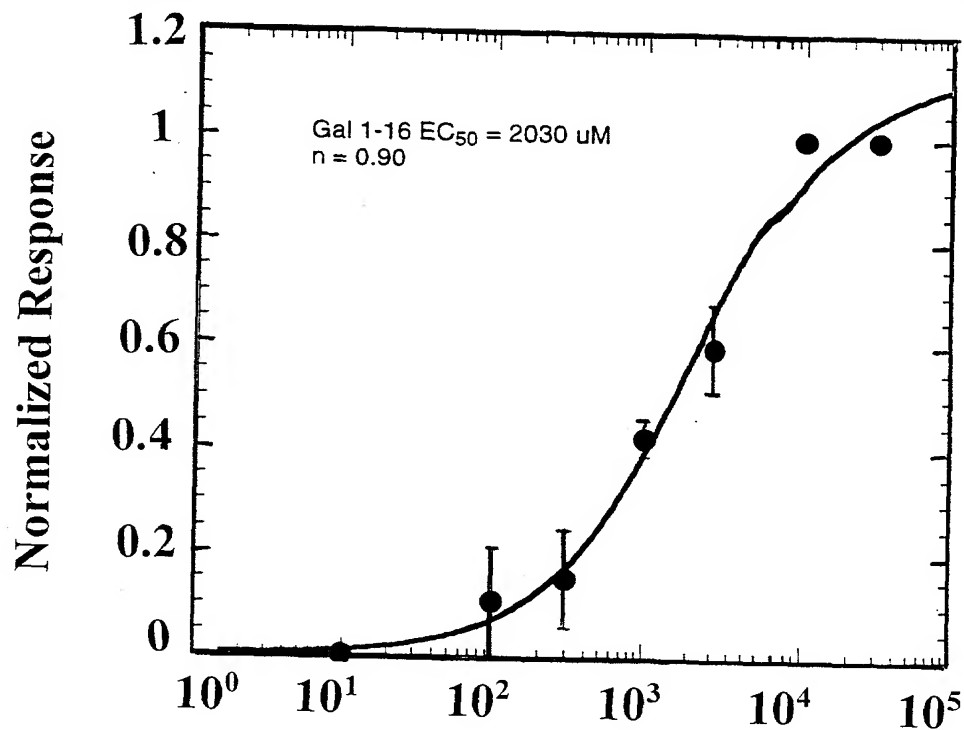
**FIGURE 8C** *12/19*



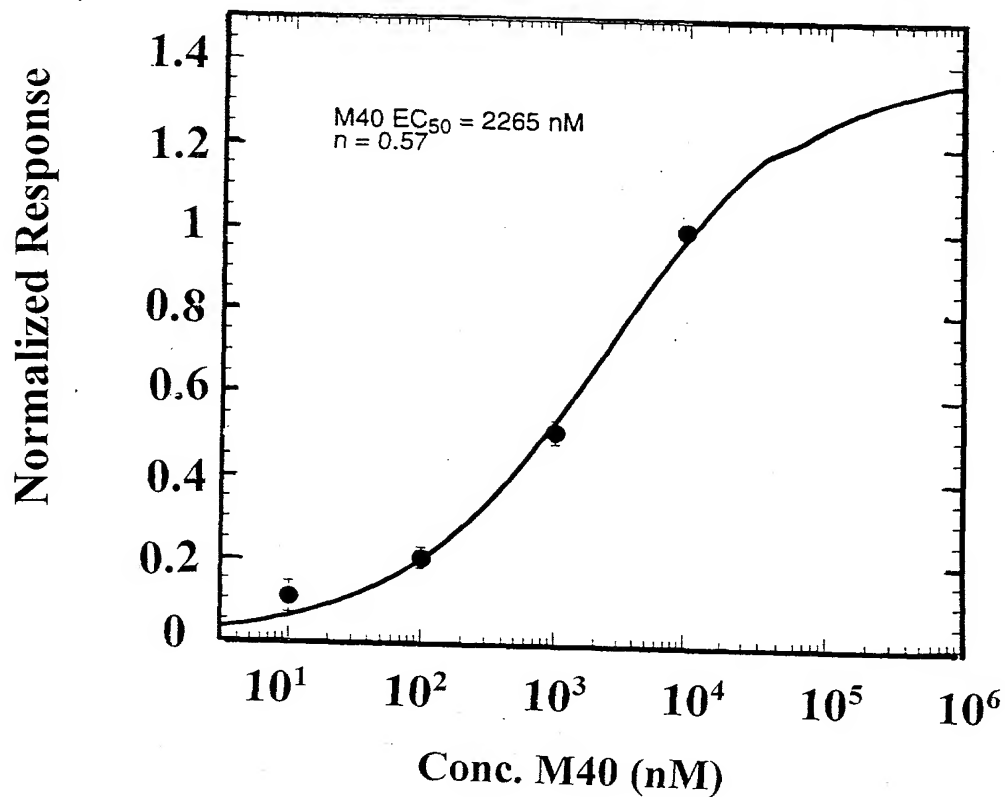
**FIGURE 8D**



**FIGURE 8E** *13/19*



**FIGURE 8F** Conc. Gal 1-16 (nM)



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FIGURE 9A

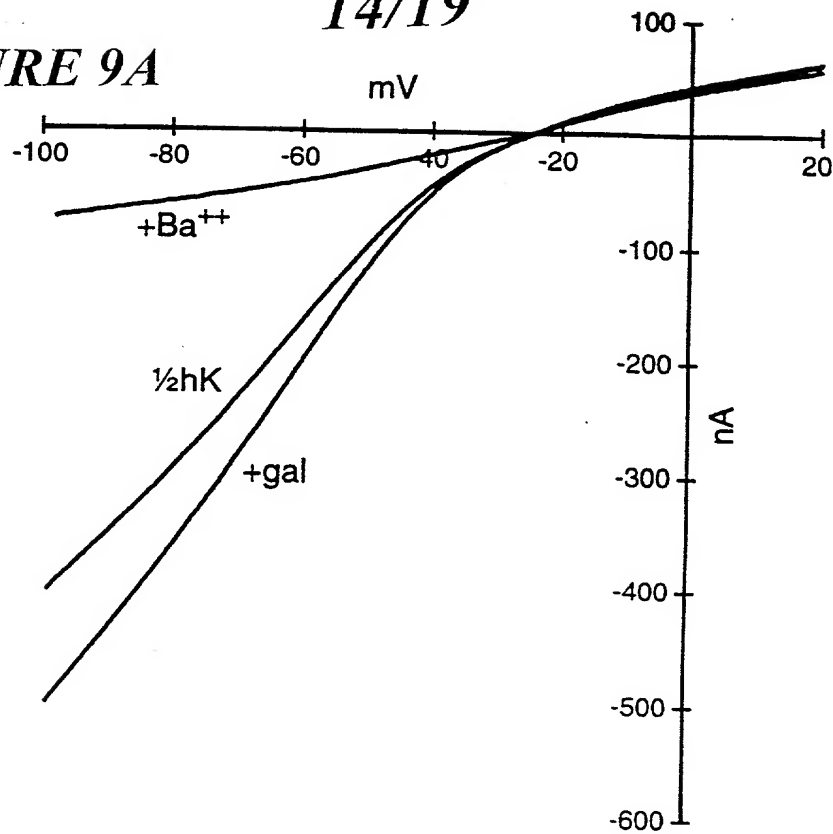
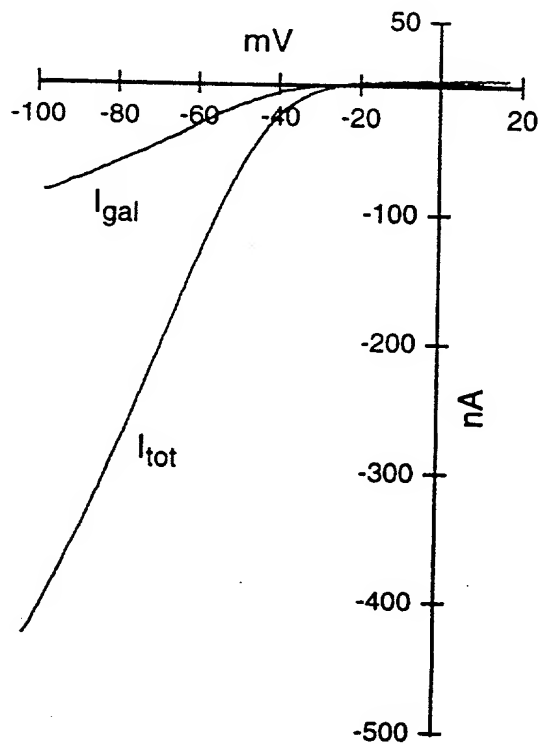


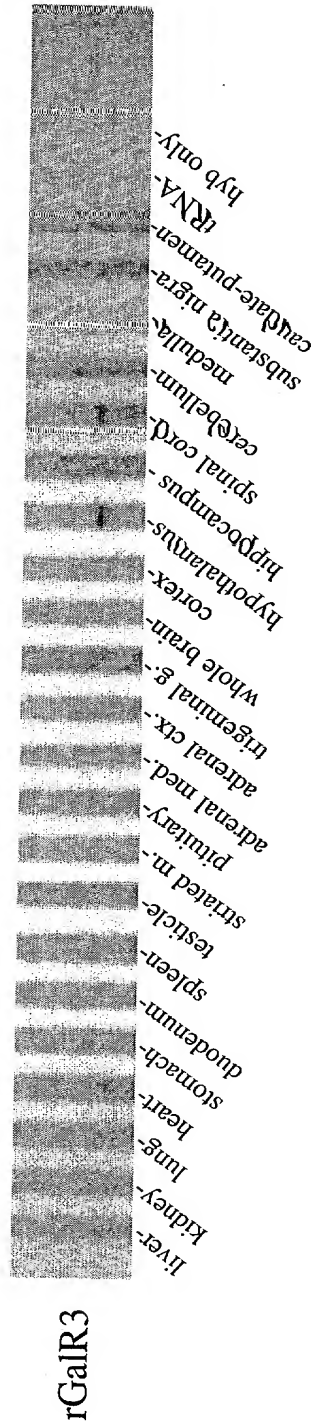
FIGURE 9B





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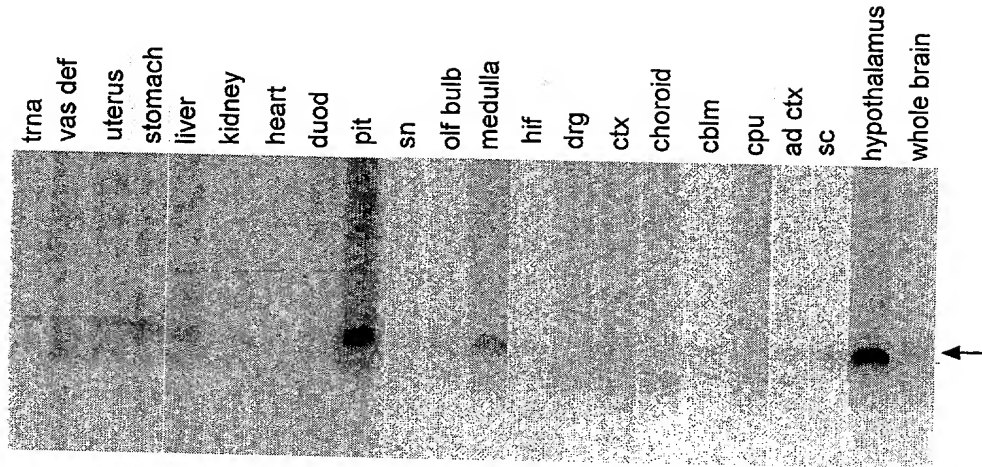
FIGURE 10



202140 1543000 F

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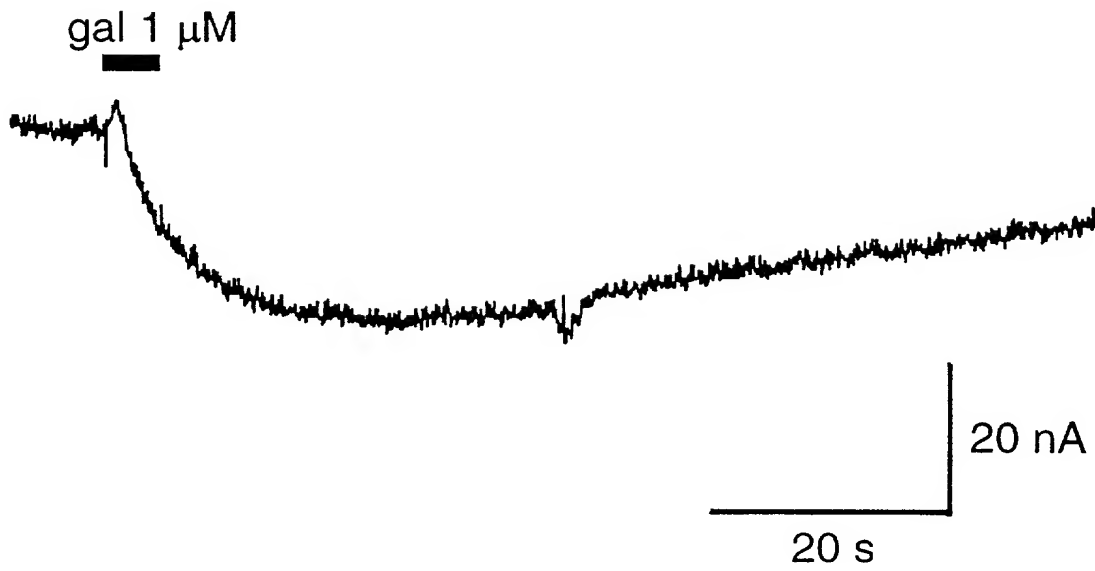
FIGURE 11





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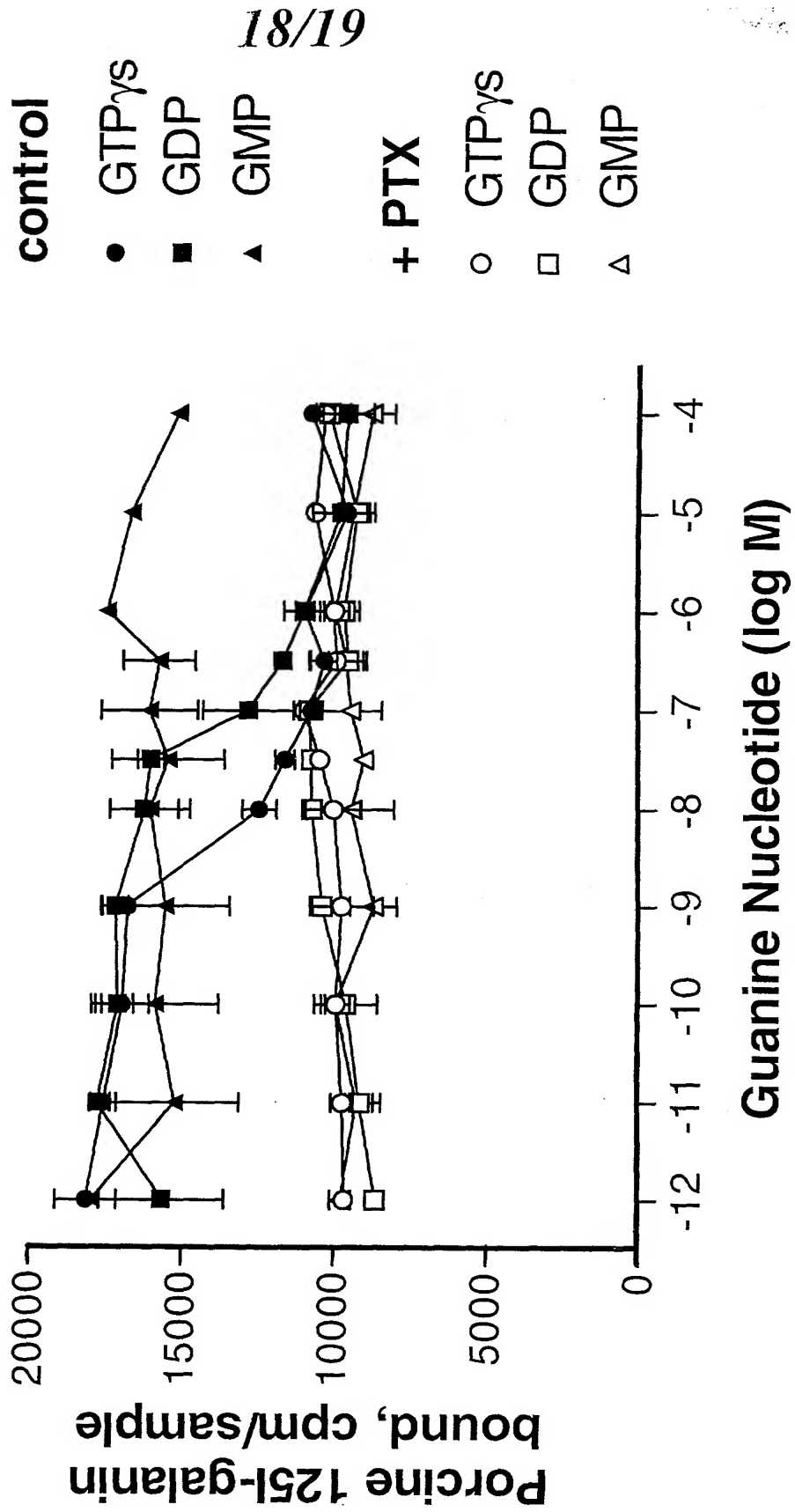
**FIGURE 12**



**FIGURE 13A**

*hGALR3-LM #228*  
 +/- *Pertussis Toxin*

**Guanine nucleotide effects**



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FIGURE 13B

